

Supplementary Information

Supplementary File 1: Identified *Salmonella* phages with accession numbers (CSV file 6.0 KB).

Supplementary File 2: Average amino acid identities of *Salmonella* phages (TSV file 79 KB).

Supplementary File 3: A shared core set of 28 orthologs from the sequences of 14 Chi-like phages (TSV file 798 KB).

Supplementary File 4: The concatenated codon-aligned nucleotide sequences of the 28 orthologs (FNA file 223 KB).

Supplementary Table S1: Complete list of *Salmonella* strains used for phage host range analysis (XLSX file 13 KB).

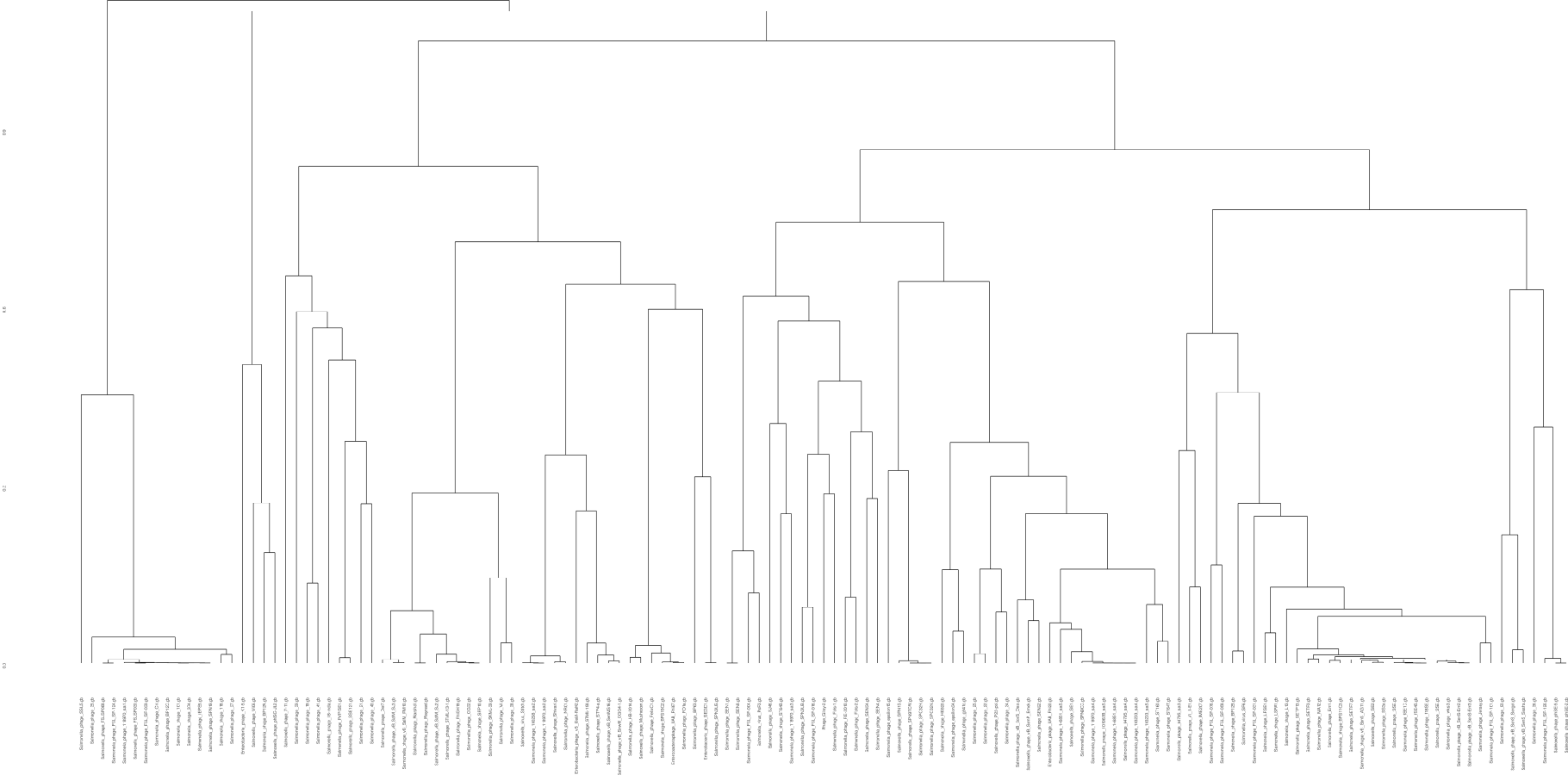
Supplementary Table S2: List of all identified *Salmonella* phages with the country of phage isolation (XLSX file 16 KB).

Supplementary Table S3: Infectivity of other Chi-like phages against 4 serovars of *Salmonella enterica* (Word Document file 15 KB).

Supplementary Table S4: List of *Salmonella* phage STm101 annotated ORFs and gene products (XLSX file 14 KB).

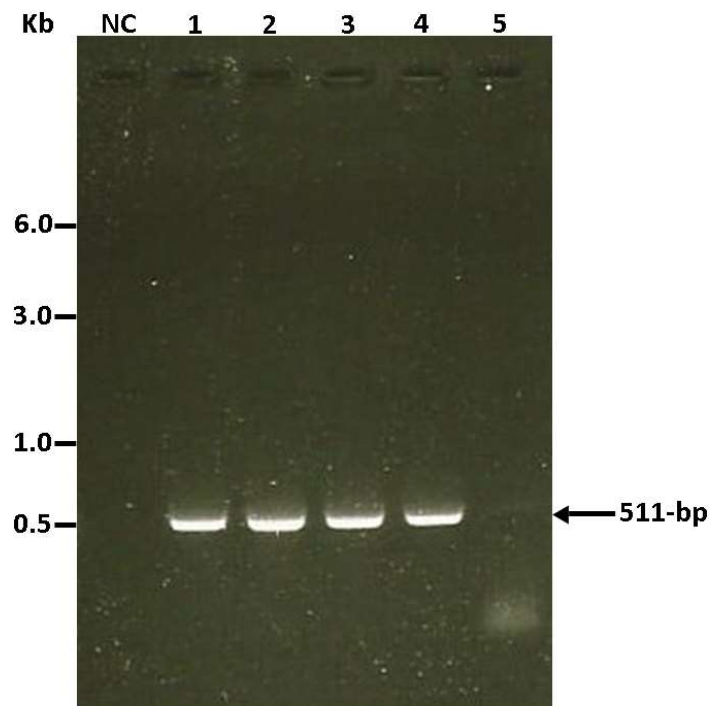
Supplementary Table S5: List of *Salmonella* phage STm118 annotated ORFs and gene products (XLSX file 15 KB).

Supplementary Figure S1



Supplementary Figure S1: A hierarchically clustering all *Salmonella* phage genomes according to their average amino acid identity.

Supplementary Figure S2



Supplementary Figure S2: 50% of all *Salmonella* phage isolates from Thai poultry farms are putative members of the Chi-like virus genus. The 511-bp PCR amplicon generated from phage DNA using primers specific for the Chi-like virus capsid protein E was visualized using 1% agarose gel electrophoresis. Positive amplification reactions are shown for STm101 (lane 1), STm118 (lane 2), STm374 (lane 3) and other Chi-like isolated phage (lane 4). Negative amplification reaction shown in lane 5 - suggesting an alternative phage type was isolated, or the primer-binding region of the capsid protein E gene sequence is different.